## SEQUENCE LISTING

110> BURNIE, JAMES PETER MATTHEWS, RUTH CHRISTINE													
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> 050885-0281578													
40> PCT/GB00/00237 41> 2000-01-28													
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<150> 09/889,314 <151> 2001-07-16													
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tct gga aaa gac aaa act tcc tcg act aca aaa aca gaa aca gct cca Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro 65 70 75 80	)												
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			gta Val									336
			gct Ala									384
			tta Leu									432
			gcg Ala 150	-	-	-	-	_				480
-		_	ttg Leu	-					_			528
			gtt Val									576
			gaa Glu	-				-			_	624
_		_	gca Ala	_						_	_	672
			gat Asp 230		_	_	_	_		 _	_	720
			tct Ser									768
			gcg Ala									816
			aca Thr									864
			gca Ala									912
			gca Ala 310									960

	gtg Val														1008
	ata Ile									_					1056
	gtc Val				-		_						_	_	1104
	gct Ala 370														1152
	gtc Val														1200
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	tcg Ser		_				_	_		_		_	_		1296
	ctg Leu														1344
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Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln 20 25 30

Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg 35 40 45

Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala 50 60

Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro 65 70 75 80

Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala 85 90 95

Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn 100 105 110

Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys 115 120 125

Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln 130 135 140

Met Lys Glu Val Glu Ala Val Val Ala Ala Leu Ser Gly Lys Ser 145 150 155 160

Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val 165 170 175

Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala 180 185 190

Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala 195 200 205

Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys 210 215 220

Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys 225 230 235 240

Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val 245 250 255

Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile 260 . 265 270

Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala 275 280 285

Gly Ala Ala Val Gly Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala 290 295 300

Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln 305 310 315 320

Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala 325 330 335

Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr 340 345 350

Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val 355 360 365

Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser 370 375 380

Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly 385 390 395 400

Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
405 410 415

Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
420 425 430

Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
435
440
445

Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Codon optimised N-terminal section of Chlamydia pneumoniae protein

<220>

<221> UNSURE

<222> (1)..(30)

<223> S-tag and thrombin cleavage site

<220>

<223> Positions (297)..(302) comprise Histidine tag

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Asp Thr Asn Met Ser Ile Ser Ser Ser Gly Pro Asp Asn Gln Lys
35 40 45

Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln 50 55 60

Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
65 70 75 80

Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala 85 90 95

Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro 100 105 110

Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala 115 120 125

Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn 130 135 140

Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys 145 150 155 160

Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
165 170 175

Met Lys Glu Val Glu Ala Val Val Ala Ala Leu Ser Gly Lys Ser 180 185 190

Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val 195 200 205

Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala 210 215 220

Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala 225 230 235 240

Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys 245 250 255

Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys 260 265 270

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Asn Thr Val Ala Ala Ala Leu Glu His His His His His 290 295 300

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Glu Lys Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr
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